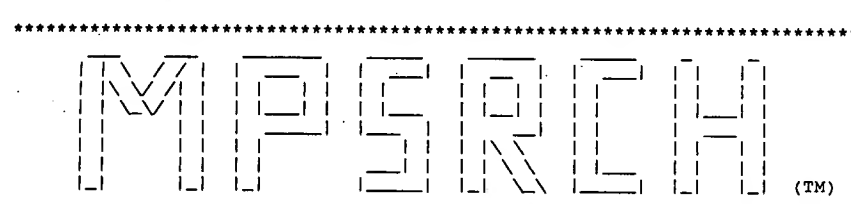

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Dec 11 06:07:02 1998; MasPar time 1448.41 Seconds
1352.597 Million cell updates/sec
Tabular output not generated.

Title: >US-08-765-588-3
Description: (1-1094) from US08765588.seq
Perfect Score: 1094
N.A. Sequence: 1 ccatgagcccctctgctccgc.....gaaggaaaaaaaaaaaaaaa 1094
Comp: ggtactcgggagacgaggcg.....cttcctttttttttttttt

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 2275026 seqs, 895388244 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: embl-est55
1:em_est1 2:em_gss1 3:em_gss2 4:em_gss3
Database: genbank-est107
5:gb_est1 6:gb_est10 7:gb_est11 8:gb_est12 9:gb_est13
10:gb_est14 11:gb_est15 12:gb_est16 13:gb_est17
14:gb_est18 15:gb_est19 16:gb_est2 17:gb_est20
18:gb_est21 19:gb_est3 20:gb_est4 21:gb_est5 22:gb_est6
23:gb_est7 24:gb_est8 25:gb_est9 26:gb_gss1 27:gb_gss2
28:gb_gss3 29:gb_gss4

Statistics: Mean 11.484; Variance 3.130; scale 3.669

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
c	1	538	49.2	565	10	AA633535	np66d06.s1 NCI_CGAP_Br	0.00e+00
c	2	510	46.6	566	18	AI141331	oy51f06.s1 NCI_CGAP_Br	0.00e+00
c	3	496	45.3	502	13	AA843665	ak08g12.s1 Soares para	0.00e+00
c	4	489	44.7	493	6	AA434389	zw31a04.s1 Soares ovar	0.00e+00
	5	483	44.1	553	11	AA082818	zn25d01.r1 Stratagene	0.00e+00
c	6	467	42.7	469	13	AA843530	ak08b11.s1 Soares para	0.00e+00
c	7	462	42.2	490	12	AA741539	ob29c01.s1 NCI_CGAP_Ki	0.00e+00
c	8	431	39.4	468	21	AA040199	zk47h01.s1 Soares preg	0.00e+00
	9	416	38.0	523	21	AA040843	zk47h01.r1 Soares preg	0.00e+00
	10	415	37.9	445	8	AA292448	zt29f01.r1 Soares ovar	0.00e+00
c	11	410	37.5	412	13	AA746258	ob08c01.s1 NCI_CGAP_Ki	0.00e+00
c	12	405	37.0	440	17	AI091655	oo19g11.x1 Soares_NSF_	0.00e+00
c	13	400	36.6	416	9	AA535588	nf87a04.s1 NCI_CGAP_Co	0.00e+00
c	14	398	36.4	402	15	AA948212	oq21f09.s1 NCI_CGAP_GC	0.00e+00
	15	387	35.4	415	24	AA310070	EST180930 Jurkat T-cel	0.00e+00
c	16	375	34.3	379	15	AA983317	oq56g10.s1 NCI_CGAP_Ki	0.00e+00
c	17	364	33.3	413	16	R56770	yg95a12.s1 Homo sapien	0.00e+00
c	18	362	33.1	372	8	AA469054	ne17d08.s1 NCI_CGAP_Co	0.00e+00
c	19	362	33.1	395	12	AA742966	ny15d03.s1 NCI_CGAP_GC	0.00e+00
	20	346	31.6	355	25	AA352350	EST60332 Activated T-c	0.00e+00
	21	342	31.3	374	22	AA182397	zp36a04.r1 Stratagene	0.00e+00
	22	316	28.9	341	16	H39505	yo54a11.r1 Homo sapien	0.00e+00
c	23	310	28.3	310	13	AA630120	ab99b07.s1 Stratagene	0.00e+00
	24	294	26.9	317	24	AA304346	EST17094 Aorta endothe	0.00e+00
	25	293	26.8	531	6	AA434485	zw31a04.r1 Soares ovar	0.00e+00
c	26	289	26.4	293	6	AA400486	zu64h12.s1 Soares test	0.00e+00
	27	287	26.2	312	16	R90829	yn02g09.r1 Homo sapien	0.00e+00
	28	283	25.9	389	18	AI174183	uc07b07.r1 Soares mous	0.00e+00
c	29	278	25.4	294	7	HUM121B07A	Human fetal brain cDNA	0.00e+00
c	30	273	25.0	299	16	H28025	yo54a11.s1 Homo sapien	0.00e+00
	31	261	23.9	297	16	R88630	ym95c03.r1 Homo sapien	0.00e+00
	32	245	22.4	279	7	HUM121B07B	Human fetal brain cDNA	0.00e+00
	33	239	21.8	289	20	N87395	L3771F Fetal heart, La	0.00e+00
	34	232	21.2	491	18	AI155033	ud78b11.r1 Soares mous	6.04e-293
c	35	226	20.7	235	15	AA932606	oo61f10.s1 NCI_CGAP_Lu	7.48e-284
	36	213	19.5	410	17	AI117413	ub78g01.r1 Soares mous	3.40e-264
	37	199	18.2	201	6	AA400532	zu64h12.r1 Soares test	4.24e-243
c	38	181	16.5	193	16	R90830	yn02g09.s1 Homo sapien	4.16e-216
	39	161	14.7	423	23	AA073660	mm94g06.r1 Stratagene	2.51e-186
	40	135	12.3	231	23	AA117672	mo61a06.r1 Stratagene	4.89e-148
	41	132	12.1	136	21	R29477	F1-621D 22 week old hu	1.17e-143
	42	124	11.3	225	5	T08411	EST06302 Homo sapiens	5.04e-132
	43	118	10.8	118	10	AA419103	zv34a01.r1 Soares ovar	2.40e-123
c	44	80	7.3	88	15	AA917955	ol68h05.s1 NCI_CGAP_Ki	1.02e-69
	45	77	7.0	381	23	AA073557	mm94h03.r1 Stratagene	1.29e-65

ALIGNMENTS

RESULT 1
LOCUS AA633535 565 bp mRNA EST 28-OCT-1997
DEFINITION np66d06.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1131275 similar to TR:G1216398 G1216398 VEGF RELATED FACTOR ISOFORM VRF167 PRECURSOR. ;, mRNA sequence.
ACCESSION AA633535
NID g2555395
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 565)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 648 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 411.
FEATURES Location/Qualifiers
source 1. .565
/organism="Homo sapiens"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified

****

MPSRCH (TM)

****

Release 3.1A John F. Collins, Biocomputing Research Unit.

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Dec 11 06:38:25 1998; MasPar time 163.86 Seconds
908.342 Million cell updates/sec
Tabular output not generated.

Title: >US-08-765-588-3
Description: (1-1094) from US08765588.seq
Perfect Score: 1094
N.A. Sequence: 1 ccatgagccctctgctccgc.....gaaggaaaaaaaaaaaaaaa 1094
Comp: ggtactcgggagacgaggcg.....cttcctttttttttttttttt

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 188442 seqs, 68026449 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40

Statistics: Mean 9.233; Variance 6.558; scale 1.408

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1094	100.0	1094	23	T33610	Vascular endothelial	0.00e+00
2	622	56.9	624	28	T37915	VEGF-B186 coding sequ	0.00e+00
3	608	55.6	910	23	T33613	Vascular endothelial	0.00e+00
4	604	55.2	666	31	T44071	Human vascular endoth	0.00e+00
5	583	53.3	993	23	T33611	Vascular endothelial	0.00e+00
6	537	49.1	1242	23	T13809	Murine VRF186 cDNA.	1.17e-297
7	496	45.3	624	28	T37914	VEGF-B186 coding sequ	5.32e-273
8	448	41.0	858	23	T33612	Vascular endothelial	3.54e-244
9	412	37.7	570	28	T37913	Fibrosarcoma VEGF-B16	1.34e-222
10	320	29.3	565	28	T37910	Adult heart VEGF-B167	1.18e-167
11	316	28.9	1141	23	T13810	Murine VRF167 cDNA.	2.83e-165
12	302	27.6	405	28	T37912	VEGF-B112 coding sequ	5.99e-157
13	241	22.0	886	28	T37909	Partial VEGF-B coding	8.07e-121
14	222	20.3	591	28	T37911	Adult heart VEGF-B174	1.26e-109
15	48	4.4	456	22	T17740	VEGF121 Cys+2 coding	3.85e-11
16	48	4.4	467	22	T17739	VEGF121 Cys+4 coding	3.85e-11
17	48	4.4	473	17	Q99080	cDNA encoding human v	3.85e-11
18	48	4.4	498	2	Q10797	Human vascular endoth	3.85e-11
19	48	4.4	599	22	T17748	VEGF165 Cys+2 coding	3.85e-11
20	48	4.4	599	22	T17747	VEGF165 Cys+4 coding	3.85e-11
21	48	4.4	605	17	Q99081	cDNA encoding human v	3.85e-11
22	48	4.4	774	33	T85644	Antisense inhibitory	3.85e-11
23	48	4.4	774	39	V15102	Human vascular endoth	3.85e-11
24	48	4.4	989	2	Q07006	Clone lambda.vegf.21	3.85e-11
25	48	4.4	1154	22	T35743	SAP-AlaMet-VEGF121 co	3.85e-11
26	48	4.4	1167	22	T17784	SAP(Gly4Ser)VEGF121 c	3.85e-11
27	48	4.4	1220	22	T35744	SAP(Gly4Ser)4VEGF121	3.85e-11
28	48	4.4	1299	22	T17785	SAP(Gly4Ser)VEGF165 c	3.85e-11
29	48	4.4	1395	22	T35740	VEGF165-AlaMet-SAP co	3.85e-11
30	48	4.4	1538	22	T35745	SAP-AlaMet-VEGF121(Gl	3.85e-11
31	48	4.4	1557	22	T17789	SAP(Gly4Ser)VEGF121(G	3.85e-11
32	48	4.4	1595	22	T35751	SAP(Gly4Ser)2VEGF121(	3.85e-11
33	48	4.4	1649	37	T95831	DNA for VEGF/CPG2 fus	3.85e-11
34	48	4.4	1664	37	T95835	DNA for VEGF/CPG2 fus	3.85e-11
35	48	4.4	1787	37	T95830	DNA for VEGF/CPG2 fus	3.85e-11
36	48	4.4	1787	22	T35749	SAP-AlaMet-VEGF165-Gl	3.85e-11
37	48	4.4	1790	37	T95832	DNA for VEGF/CPG2 fus	3.85e-11
38	48	4.4	1790	37	T95833	DNA for VEGF/CPG2 fus	3.85e-11
39	48	4.4	1802	22	T35748	SAP-AlaMet-VEGF165(Gl	3.85e-11
40	48	4.4	1808	22	T35752	SAP-GlySer-VEGF165(Gl	3.85e-11
41	48	4.4	1809	22	T17790	SAP(Gly4Ser)VEGF165(G	3.85e-11
42	48	4.4	1823	22	T35750	SAP-AlaMet-VEGF165(Gl	3.85e-11
43	48	4.4	1832	37	T95834	DNA for VEGF/CPG2 fus	3.85e-11
44	48	4.4	1859	22	T35753	SAP(Gly4Ser)2VEGF165(	3.85e-11
45	48	4.4	1873	39	V15103	Human vascular endoth	3.85e-11

ALIGNMENTS

RESULT 1
ID T33610 standard; cDNA; 1094 BP.
AC T33610;
DT 30-NOV-1996 (first entry)
DE Vascular endothelial growth factor-like protein SOM175 cDNA.
KW Vascular endothelial growth factor; VEGF; VEGF165; SOM175; neuron;
KW astroglial proliferation; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 3..626
FT /*tag= a
FT signal_peptide 3..65
FT /*tag= b
FT mat_peptide 66..623
FT /*tag= c
PN WO9627007-A1.
PD 06-SEP-1996.
PF 22-FEB-1996; AU0094.
PR 02-MAR-1995; AU-001457.
PR 20-NOV-1995; AU-006647.
PR 22-DEC-1995; AU-007274.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PI Grimmond S, Hayward NK, Larsson C, Nordenskjold M;
PI Weber G;
DR WPI; 96-412774/41.
DR P-PSDB; W00725.
PT New growth factor related to vascular endothelial growth factor -
PT useful for inducing astroglial proliferation and promoting neuronal
PT survival
PS Claim 32; Page 39-40; 113pp; English.
CC SOM175 cDNA (T33610) codes for a human vascular endothelial growth
CC factor (VEGF)-like polypeptide (W00725) capable of inducing
CC astroglial proliferation and of promoting neural survival and/or
CC proliferation. It was isolated by screening a human foetal brain
CC library with the cosmid D11S750. Nucleotide sequence homology to
CC the human VEGF gene (see also T33609) is 69.7%. The SOM175 gene
CC maps to human chromosome 11q13. Splice variants of SOM175 (see

****

MPsrch (TM)

****

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Dec 11 05:32:48 1998; MasPar time 1605.71 Seconds
1501.485 Million cell updates/sec

Tabular output not generated.

Title: >US-08-765-588-3
Description: (1-1094) from US08765588.seq
Perfect Score: 1094
N.A. Sequence: 1 ccatgagccctctgctccgc.....gaaggaaaaaaaaaaaaaaa 1094
Comp: ggtactcgggagacgaggcg.....cttccttttttttttttttt

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 567134 seqs, 1101898692 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: embl55
1:em_ba 2:em_fun 3:em_htg 4:em_hum1 5:em_hum2 6:em_in
7:em_om 8:em_or 9:em_ov 10:em_pat 11:em_ph 12:em_pl
13:em_ro 14:em_vi
Database: genbank107
15:gb_ba1 16:gb_ba2 17:gb_htg 18:gb_in 19:gb_om 20:gb_ov
21:gb_pat 22:gb_ph 23:gb_pl1 24:gb_pl2 25:gb_pr1
26:gb_pr2 27:gb_pr3 28:gb_ro 29:gb_st 30:gb_sts 31:gb_sy
32:gb_un 33:gb_vi

Statistics: Mean 11.281; Variance 6.527; scale 1.728

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
	1	1079	98.6	1079	25	HSU43368	Human VEGF related fac	0.00e+00
	2	749	68.5	755	27	HSU52819	Human vascular endothe	0.00e+00
	3	545	49.8	896	28	MMU52820	Mus musculus vascular	0.00e+00
	4	545	49.8	1236	28	MMU43836	Mus musculus VEGF-rela	0.00e+00
	5	412	37.7	570	25	HSU48801	Human vascular endothe	1.34e-267
	6	412	37.7	570	21	I36629	Sequence 10 from paten	1.34e-267
	7	410	37.5	567	25	HSU43369	Human VEGF related fac	3.88e-266
c	8	364	33.3	413	30	G21825	human STS WI-14122.	1.46e-232
	9	324	29.6	795	28	MMU48800	Mus musculus vascular	1.80e-203
	10	322	29.4	567	28	MMU43837	Mus musculus VEGF-rela	5.10e-202
	11	320	29.3	565	21	I36626	Sequence 4 from patent	1.44e-200
	12	302	27.6	405	21	I36628	Sequence 8 from patent	1.61e-187
	13	283	25.9	349	28	AF032925	Rattus norvegicus vasc	8.87e-174
	14	248	22.7	453	28	AF022952	Rattus norvegicus vasc	1.45e-148
	15	241	22.0	886	21	I36625	Sequence 1 from patent	1.54e-143
	16	222	20.3	591	21	I36627	Sequence 6 from patent	6.19e-130
	17	67	6.1	7218	21	I66494	Sequence 14 from paten	3.73e-23
	18	56	5.1	226	19	AF022179	Oryctolagus cuniculus	2.53e-16
c	19	52	4.8	7218	21	I66494	Sequence 14 from paten	6.59e-14
	20	50	4.6	576	25	S82167	simVEGF165=vascular en	1.02e-12
	21	48	4.4	576	21	A64392	Sequence 5 from Patent	1.54e-11
	22	48	4.4	630	27	HSA010438	Homo sapiens mRNA for	1.54e-11
	23	48	4.4	649	25	HSVEGF	H.sapiens vegf gene fo	1.54e-11
	24	48	4.4	774	21	E13215	Human mRNA for vascula	1.54e-11
	25	48	4.4	774	10	E11017	A part of pSU 2 includ	1.54e-11
	26	48	4.4	774	21	E13332	cDNA encoding vascular	1.54e-11
	27	48	4.4	815	27	S85192	Homo sapiens vascular	1.54e-11
	28	48	4.4	990	25	HUMEGFAA	Human heparin-binding	1.54e-11
	29	48	4.4	1195	25	HUMVPF	Human vascular permeab	1.54e-11
	30	48	4.4	1649	21	A64396	Sequence 9 from Patent	1.54e-11
	31	48	4.4	1664	21	A64404	Sequence 17 from Paten	1.54e-11
	32	48	4.4	1787	21	A64394	Sequence 7 from Patent	1.54e-11
	33	48	4.4	1790	21	A64398	Sequence 11 from Paten	1.54e-11
	34	48	4.4	1790	21	A64400	Sequence 13 from Paten	1.54e-11
	35	48	4.4	1832	21	A64402	Sequence 15 from Paten	1.54e-11
	36	47	4.3	105	25	HSU43370	Human VEGF related fac	5.91e-11
	37	46	4.2	3166	27	AF022375	Homo sapiens vascular	2.25e-10
	38	44	4.0	231	25	HUMVEGF3	Human vascular endothe	3.18e-09
	39	44	4.0	573	19	SSVEGF	S.scrofa mRNA for vasc	3.18e-09
	40	42	3.8	495	28	GPIVEGFA	Guinea pig vascular en	4.32e-08
	41	42	3.8	802	19	BOVVEGFB	Bovine vascular endoth	4.32e-08
	42	42	3.8	934	19	BOVVEGFA	Bovine vascular endoth	4.32e-08
	43	42	3.8	1536	19	BOVEGFA	Bovine heparin-binding	4.32e-08
	44	40	3.7	573	19	AF071015	Ovis aries vascular en	5.65e-07
	45	40	3.7	589	28	S38083	vascular endothelial g	5.65e-07

ALIGNMENTS

RESULT 1
LOCUS HSU43368 1079 bp mRNA PRI 07-MAR-1996
DEFINITION Human VEGF related factor isoform VRF186 precursor (VRF) mRNA, complete cds.
ACCESSION U43368
NID g1216395
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1079)
AUTHORS Grimmond,S., Lagercrantz,J., Drinkwater,C., Silins,G., Townson,S., Pollock,P., Gotley,D., Carson,E., Rakar,S., Nordenskjold,M., Ward,L., Hayward,N. and Weber,G.
TITLE Cloning and characterization of a novel human gene related to vascular endothelial growth factor
JOURNAL Genome Res. 6 (2), 122-129 (1996)
REFERENCE 2 (bases 1 to 1079)
AUTHORS Silins,G.U.
TITLE Direct Submission
JOURNAL Submitted (15-DEC-1995) Ginters U. Silins, Human Genetics, Queensland Institute of Medical Research, Herston, Queensland, 4029, Australia
FEATURES Location/Qualifiers
source 1. .1079
/organism="Homo sapiens"
/note="GDB DSEG number=D11S750"
/db_xref="taxon:9606"
/clone_lib="Human fetal brain cDNA library from Stratagene"
/map="11q13"
/chromosome="11"
/tissue_type="brain"
/dev_stage="fetus"
gene 3. .626
/gene="VRF"

****

MPSRCH (TM)

****

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Dec 11 06:42:18 1998; MasPar time 43.51 Seconds
1172.855 Million cell updates/sec

Tabular output not generated.

Title: >US-08-765-588-3
Description: (1-1094) from US08765588.seq
Perfect Score: 1094
N.A. Sequence: 1 ccatgagccctctgctccgc.....gaaggaaaaaaaaaaaaaaa 1094
Comp: ggtactcgggagacgaggcg.....cttcctttttttttttttt

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 88822 seqs, 23323279 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-issued
1:5_COMB 2:PCT9_COMB 3:backfiles1

Statistics: Mean 8.813; Variance 5.776; scale 1.526

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
	1	412	37.7	570	1	US-08-469-	Sequence 10, Applicati	7.79e-243
	2	320	29.3	565	1	US-08-469-	Sequence 4, Applicatio	3.12e-183
	3	302	27.6	405	1	US-08-469-	Sequence 8, Applicatio	1.29e-171
	4	241	22.0	886	1	US-08-469-	Sequence 1, Applicatio	2.08e-132
	5	222	20.3	591	1	US-08-469-	Sequence 6, Applicatio	2.92e-120
	6	67	6.1	7218	1	US-08-232-	Sequence 14, Applicati	5.56e-24
c	7	52	4.8	7218	1	US-08-232-	Sequence 14, Applicati	2.15e-15
	8	48	4.4	456	2	PCT-US95-1	Sequence 88, Applicati	3.61e-13
	9	48	4.4	467	2	PCT-US95-1	Sequence 86, Applicati	3.61e-13
	10	48	4.4	473	2	PCT-US95-1	Sequence 25, Applicati	3.61e-13
	11	48	4.4	498	3	5194596-20	Patent No. 5194596.	3.61e-13
	12	48	4.4	599	2	PCT-US95-1	Sequence 89, Applicati	3.61e-13
	13	48	4.4	599	2	PCT-US95-1	Sequence 87, Applicati	3.61e-13
	14	48	4.4	605	2	PCT-US95-1	Sequence 26, Applicati	3.61e-13
	15	48	4.4	989	3	5332671-11	Patent No. 5332671.	3.61e-13
	16	48	4.4	1167	2	PCT-US95-1	Sequence 57, Applicati	3.61e-13
	17	48	4.4	1195	3	5240848-6	Patent No. 5240848.	3.61e-13
	18	48	4.4	1212	2	PCT-US95-1	Sequence 31, Applicati	3.61e-13
	19	48	4.4	1269	2	PCT-US95-1	Sequence 32, Applicati	3.61e-13
	20	48	4.4	1299	2	PCT-US95-1	Sequence 58, Applicati	3.61e-13
	21	48	4.4	1369	2	PCT-US95-1	Sequence 33, Applicati	3.61e-13
	22	48	4.4	1557	2	PCT-US95-1	Sequence 78, Applicati	3.61e-13
	23	48	4.4	1809	2	PCT-US95-1	Sequence 79, Applicati	3.61e-13
	24	47	4.3	677	2	PCT-US95-1	Sequence 27, Applicati	1.28e-12
	25	47	4.3	728	2	PCT-US95-1	Sequence 28, Applicati	1.28e-12
	26	46	4.2	498	3	5219739-21	Patent No. 5219739.	4.53e-12
	27	44	4.0	197	2	PCT-US95-1	Sequence 18, Applicati	5.56e-11
	28	44	4.0	886	3	5219739-23	Patent No. 5219739.	5.56e-11
	29	42	3.8	789	3	5219739-8	Patent No. 5219739.	6.67e-10
	30	42	3.8	790	3	5194596-8	Patent No. 5194596.	6.67e-10
	31	42	3.8	961	3	5219739-16	Patent No. 5219739.	6.67e-10
	32	42	3.8	1543	3	5332671-5	Patent No. 5332671.	6.67e-10
	33	38	3.5	215	1	US-08-238-	Sequence 5, Applicatio	8.79e-08
c	34	38	3.5	215	1	US-08-238-	Sequence 5, Applicatio	8.79e-08
	35	38	3.5	961	3	5194596-16	Patent No. 5194596.	8.79e-08
c	36	28	2.6	5775	2	PCT-US93-0	Sequence 29, Applicati	9.16e-03
	37	27	2.5	242	1	US-08-273-	Sequence 1, Applicatio	2.72e-02
	38	26	2.4	2504	1	US-08-484-	Sequence 15, Applicati	7.93e-02
	39	26	2.4	2504	1	US-08-484-	Sequence 15, Applicati	7.93e-02
	40	26	2.4	5011	1	US-08-141-	Sequence 1, Applicatio	7.93e-02
c	41	25	2.3	6513	2	PCT-US95-1	Sequence 7, Applicatio	2.28e-01
c	42	25	2.3	6513	2	PCT-US95-1	Sequence 7, Applicatio	2.28e-01
c	43	25	2.3	6513	1	US-08-337-	Sequence 7, Applicatio	2.28e-01
c	44	25	2.3	6513	1	US-08-724-	Sequence 7, Applicatio	2.28e-01
c	45	25	2.3	8438	1	US-07-945-	Sequence 1, Applicatio	2.28e-01

ALIGNMENTS

RESULT 1
ID US-08-469-427A-10 STANDARD; DNA; UNC; 570 BP.
AC xxxxxx
DT
DE Sequence 10, Application US/08469427A
CC Sequence 10, Application US/08469427A
CC Patent No. 5607918
CC GENERAL INFORMATION:
CC APPLICANT: Eriksson, Ulf
CC APPLICANT: Olofsson, Birgitta
CC APPLICANT: Alitalo, Kari
CC APPLICANT: Pajusola, Katri
CC TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
CC TITLE OF INVENTION: DNA CODING THEREFOR
CC NUMBER OF SEQUENCES: 17
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
CC STREET: 1200 G Street, N.W., Suite 700
CC CITY: Washington
CC STATE: DC
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/469,427A
CC FILING DATE: 06-JUN-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/397,651
CC FILING DATE: 01-MAR-1995
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Evans, Joseph D
CC REGISTRATION NUMBER: 26,269
CC REFERENCE/DOCKET NUMBER: 41979cp2
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (202) 628-8800
CC TELEFAX: (202) 628-8844
CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 570 base pairs
CC TYPE: nucleic acid

****

MPSRCH (TM)

****

Release 3.1A John F. Collins, Biocomputing Research Unit.

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Dec 11 06:43:42 1998; MasPar time 917.76 Seconds
1290.001 Million cell updates/sec

Tabular output not generated.

Title: >US-08-765-588-3
Description: (1-1094) from US08765588.seq
Perfect Score: 1094
N.A. Sequence: 1 ccatgagccctctgctccgc.....gaaggaaaaaaaaaaaaaaa 1094
Comp: ggtactcgggagacgaggcg.....cttccttttttttttttttt

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 1686833 seqs, 541095398 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-pending
1:P9 2:U6000 3:U6001 4:U6002 5:U6003 6:U6004 7:U6005
8:U6006 9:U6007 10:U6008 11:U7 12:U80 13:U81 14:U82
15:U83 16:U84A 17:U84B 18:U85 19:U86 20:U87 21:U88
22:U89 23:U90A 24:U90B 25:U91 26:NEWP 27:NEWU6 28:NEWU8
29:NEWU9

Statistics: Mean 10.542; Variance 4.383; scale 2.405

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1094	100.0	1094	28	US-	Sequence 3, Applicatio	0.00e+00
2	622	56.9	624	19	US-	Sequence 14, Applicati	0.00e+00
3	622	56.9	624	18	US-	Sequence 14, Applicati	0.00e+00
4	622	56.9	624	19	US-	Sequence 14, Applicati	0.00e+00
5	622	56.9	624	18	US-	Sequence 14, Applicati	0.00e+00
6	622	56.9	624	18	US-	Sequence 14, Applicati	0.00e+00
7	608	55.6	910	28	US-	Sequence 9, Applicatio	0.00e+00
8	604	55.2	666	25	US-	Sequence 1, Applicatio	0.00e+00
9	604	55.2	666	23	US-	Sequence 1, Applicatio	0.00e+00
10	604	55.2	666	17	US-	Sequence 1, Applicatio	0.00e+00
11	604	55.2	666	17	US-	Sequence 1, Applicatio	0.00e+00
12	583	53.3	993	28	US-	Sequence 5, Applicatio	0.00e+00
13	537	49.1	1242	28	US-	Sequence 16, Applicati	0.00e+00
14	496	45.3	624	19	US-	Sequence 12, Applicati	0.00e+00
15	496	45.3	624	18	US-	Sequence 12, Applicati	0.00e+00
16	496	45.3	624	19	US-	Sequence 12, Applicati	0.00e+00
17	496	45.3	624	18	US-	Sequence 12, Applicati	0.00e+00
18	496	45.3	624	18	US-	Sequence 12, Applicati	0.00e+00
19	448	41.0	858	28	US-	Sequence 7, Applicatio	0.00e+00
20	412	37.7	570	19	US-	Sequence 10, Applicati	0.00e+00
21	412	37.7	570	17	US-	Sequence 10, Applicati	0.00e+00
22	412	37.7	570	18	US-	Sequence 10, Applicati	0.00e+00
23	412	37.7	570	18	US-	Sequence 10, Applicati	0.00e+00
24	412	37.7	570	18	US-	Sequence 10, Applicati	0.00e+00
25	412	37.7	570	19	US-	Sequence 10, Applicati	0.00e+00
26	346	31.6	355	13	US-	Sequence 3430, Applica	0.00e+00
27	346	31.6	355	13	US-	Sequence 3430, Applica	0.00e+00
28	320	29.3	565	17	US-	Sequence 4, Applicatio	2.06e-282
29	320	29.3	565	18	US-	Sequence 4, Applicatio	2.06e-282
30	320	29.3	565	19	US-	Sequence 4, Applicatio	2.06e-282
31	320	29.3	565	18	US-	Sequence 4, Applicatio	2.06e-282
32	320	29.3	565	19	US-	Sequence 4, Applicatio	2.06e-282
33	320	29.3	565	18	US-	Sequence 4, Applicatio	2.06e-282
34	320	29.3	565	17	US-	Sequence 4, Applicatio	2.06e-282
35	308	28.2	313	21	US-	Sequence 1619, Applica	2.78e-270
36	309	28.2	363	20	US-	Sequence 239, Applicat	2.72e-271
37	302	27.6	405	19	US-	Sequence 8, Applicatio	3.19e-264
38	302	27.6	405	19	US-	Sequence 8, Applicatio	3.19e-264
39	302	27.6	405	17	US-	Sequence 8, Applicatio	3.19e-264
40	302	27.6	405	18	US-	Sequence 8, Applicatio	3.19e-264
41	302	27.6	405	17	US-	Sequence 8, Applicatio	3.19e-264
42	302	27.6	405	18	US-	Sequence 8, Applicatio	3.19e-264
43	302	27.6	405	18	US-	Sequence 8, Applicatio	3.19e-264
44	300	27.4	346	22	US-	Sequence 3606, Applica	3.33e-262
45	285	26.1	414	21	US-	Sequence 2393, Applica	4.45e-247

ALIGNMENTS

RESULT 1
ID US-08-765-588-3 STANDARD; DNA; UNC; 1094 BP.
AC xxxxxx
DT
DE Sequence 3, Application US/08765588
CC Sequence 3, Application US/08765588
CC GENERAL INFORMATION:
CC APPLICANT: Hayward, Nicholas K.
CC APPLICANT: Weber, Gunther
CC APPLICANT: Grimmond, Sean
CC APPLICANT: Nordenskjold, Magnus
CC APPLICANT: Larsson, Catharina
CC TITLE OF INVENTION: A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING
CC TITLE OF INVENTION: SAME
CC FILE REFERENCE: DAVIES
CC CURRENT APPLICATION NUMBER: US/08/765,588
CC CURRENT FILING DATE: 1997-04-25
CC NUMBER OF SEQ ID NOS: 23
CC SOFTWARE: PatentIn Ver. 2.0
CC SEQ ID NO 3
CC LENGTH: 1094
CC TYPE: DNA
CC ORGANISM: Nucleotide Sequence of SOM175
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: (3)..(623)
SQ SEQUENCE 1094 BP; 245 A; 359 C; 300 G; 190 T; 0 OTHER.

Query Match 100.0%; Score 1094; DB 28; Length 1094;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 1094; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Db      1 CCATGAGCCCTCTGCTCCGCCGCCTGCTGCTCGCCGCACTCCTGCAGCTGGCCCCCGCCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1 ccatgagccctctgctccgccgcctgctgctcgccgcactcctgcagctggccccgccc 60

Db     61 AGGCCCCTGTCTCCCAGCCTGATGCCCCTGGCCACCAGAGGAAAGTGGTGTCATGGATAG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 aggcccctgtctcccagcctgatgcccctggccaccagaggaaagtggtgtcatggatag 120
```

Saoud, Christine
To: STIC-Biotech/ChemLib
Subject: 08/765588

Sequence search –

Please return results via SCORE.

SEQ ID NO:4, 8, 10. – protein search. Patent database – issued and pending.
SEQ ID NO:16 and 3 – nucleic acids. Patent database – issued and pending.

Thank you,
Christine Saoud
AU 1647
571-272-0891
REM 04E81

12-[redacted]927

STIC-Biotech/ChemLib

From: Elliott, George
Sent: Wednesday, December 30, 1998 3:18 PM
To: STIC-Biotech/ChemLib
Cc: Saoud, Christine
Subject: FW: RUSH search

Importance: High

Please rush.

Thanks,

George

-----Original Message-----
From: Saoud, Christine
Sent: Wednesday, December 30, 1998 2:18 PM
To: Elliott, George
Subject: RUSH search
Importance: High

u.S.S.N. 08/765,588

Please search SEQ ID NO:16 in the patent and commercial databases.
This is a rush search because it is a due amended.

thank you,
christine Saoud
CM1-10E03
305-7519